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DESCRIPTION

siRNA CAPABLE OF INHIBITING EXPRESSION OF WT1 GENE AND USE THEREOF

Technical Field

The present invention relates to siRNA that suppresses the expression of WT1 gene and uses thereof. In particular, the present invention relates to suppression of cell growth and induction of cell death using such siRNA.

Background Art

Wilms tumor gene (WT1 gene) is a zinc-finger transcription factor-encoding gene. WT1 gene is known to have four isoforms distinguished by the presence or absence of 17 amino acids (17AA) inserted at the 5'-side site of the two alternative splicing sites of the gene, as well as by the presence or absence of three amino acid residues between zinc fingers 3 and 4.

Wilms tumor gene (WT1 gene) was isolated as a causative gene of pediatric kidney tumor (Non-patent Documents 1 and 2). Since some deletions and mutations in this gene have been found in Wilms tumor, it has been believed that this gene is a tumor suppressor gene.

However, a number of reports by the present inventors suggest that WT1 gene exerts an oncogene-like function rather than functions as a tumor suppressor gene. It has been revealed that almost all leukemia cells express high levels of the nonmutated wild type WT1 gene, and the expression level in leukemia is reciprocally correlated with the prognosis of patients (Non-patent Documents 3 and 4); antisense WT1 DNA specifically suppresses the growth of leukemia cells (Non-patent Document 5); forced expression of the WT1 gene results in suppression of the differentiation of mouse normal bone marrow precursor cells and bone marrow precursor cell line 32D C13 into neutrophils, and the cells began proliferating as a result (Non-patent Document 6); *etc.* These findings suggest that the WT1 gene is involved in the leukemogenic conversion of hematopoietic cells. The present inventors have also reported that the wild type WT1 gene is expressed at high levels in various types of solid cancers (Non-patent Documents 7 to 14).

The present inventors believe that the WT1 gene would be useful for the development of tumor-specific molecular target therapy if expression of the gene can be efficiently suppressed. To date, no tumor-specific molecular target therapy that targets WT1 has been known.

[Non-patent Document 1] Call KM, *et al.*: Isolation and characterization of a zinc finger polypeptide gene at the human chromosome 11 Wilms' tumor locus. Cell 60: 509, 1990

[Non-patent Document 2] Gessler M, *et al.*: Homozygous deletion in Wilms tumours of a

zinc-finger gene identified by chromosome jumping. Nature 343 '. 774, 1990

[Non-patent Document 3] Inoue K, *et al.*: WTl as a new prognostic factor and a new marker for the detection of minimal residual disease in acute leukemia. Blood 84: 3071, 1994

[Non-patent Document 4] Inoue K, *et al.*: Aberrant overexpression of the Wilms tumor gene (WT1) in human leukemia. Blood 89: 1405, 1997

[Non-patent Document 5] Yamagami T, Sugiyama H, Inoue K, Ogawa H, Tatekawa T, Hirata M, Kudoh T, Akiyama T, Murakami A, Maekawa T. Growth inhibition of human leukemic cells by WT1 (Wilms tumor gene) antisense oligodeoxynucleotides: implications for the involvement of WT1 in leukemogenesis. Blood. 1996 Apr 1;87(7):2878-84.

[Non-patent Document 6] Inoue K, *et al.*: Wilms' tumor gene (WTl) competes with differentiation-inducing signal in hematopoietic progenitor cells. Blood 91:2969,1998

[Non-patent Document 7] Oji, Y., Ogawa, H., Tamaki, H., Oka, Y., Tsuboi, A., Kim, E.H., Soma, T., Tatekawa, T., Kawakami, M., Asada, M., Kishimoto, T., and Sugiyama, H. Expression of the Wilms' tumor gene WT1 in solid tumors and its involvement in tumor cell growth. Japanese Journal of Cancer Research, 90: 194-204, 1999.

[Non-patent Document 8] Oji, Y., Miyoshi, S., Maeda, H., Hayashi, S., Tamaki, H., Nakatsuka, S., Yao, M., Takahashi, E., Nakano, Y., Hirabayashi, H., Shintani, Y., Oka, Y., Tsuboi, A., Hosen, N., Asada, M., Fujioka, T., Murakami, M., Kanato, K., Motomura, M., Kim, E.H., Kawakami, M., Ikegame, K., Ogawa, H., Aozasa, K., Kawase, I., and Sugiyama, H. Overexpression of the Wilms' tumor gene WT1 in de novo lung cancers. International Journal of Cancer, 100: 304-308, 2002.

[Non-patent Document 9] Ueda, T., Oji, Y., Naka, N., Nakano, Y., Takahashi, E., Koga, S., Asada, M., Ikeba, A., Nakatsuka, S., Abeno, S., Hosen, N., Tomita, Y., Aozasa, K., Tamai, N., Myoui, A., Yoshikawa, H., and Sugiyama, H. Overexpression of the Wilms' tumor gene WT1 in human bone and soft-tissue sarcomas. Cancer Science, 94: 271-276, 2003.

[Non-patent Document 10] Oji, Y., Inohara, H., Nakazawa, M., Nakano, Y., Akahani, S., Nakatusuka, S., Koga, S., Abeno, S., Honjo, Y., Yamamoto, Y., Iwai, S., Yoshida, K., Oka, Y., Ogawa, H., Yoshida, J., Aozasa, K., Kubo, T., and Sugiyama, H. Overexpression of the Wilms' tumor gene WT1 in head and neck squamous cell carcinoma. Cancer Science, 94: 523-529, 2003.

[Non-patent Document 11] Oji, Y., Miyoshi, Y., Koga, S., Nakano, Y., Ando, A., Nakatuska, S., Ikeba, A., Takahashi, E., Sakaguchi, N., Yokota, A., Hosen, N., Ikegame, K., Kawakami, M., Tsuboi, A., Oka, Y., Ogawa, H., Aozasa, K., Noguchi, S., and Sugiyama, H. Overexpression of the Wilms' tumor gene WT1 in primary thyroid cancer. Cancer Science, 94: 606-611, 2003.

[Non-patent Document 12] Oji, Y., Yamamoto, H., Nomura, M., Nakano, Y., Ikeba, A., Nakatsuka, S., Abeno, S., Kiyotoh, E., Jomgeow, T., Sekimoto, M., Nezu, R., Yoshikawa, Y., Inoue, Y., Hosen, N., Kawakami, M., Tsuboi, A., Oka, Y., Ogawa, H., Souda, S., Aozasa, K.,

Monden, M., and Sugiyama, H. Overexpression of the Wilms' tumor gene WT1 in colorectal adenocarcinoma. Cancer Science, 94: 712-717, 2003.

[Non-patent Document 13] Oji, Y., Miyoshi, S., Takahashi, E., Koga, S., Nakano, Y., Shintani, Y., Hirabayashi, H., Matsumura, A., Iuchi, K., Ito, K., Kishimoto, Y., Tsuboi, A., Ikegame, K., Hosen, N., Oka, Y., Ogawa, H., Maeda, H., Hayashi, S., Kawase, I., and Sugiyama, H. Absence of mutations in the Wilms' tumor gene WT1 in de novo non-small cell lung cancers. Neoplasma, 51:17-20, 2004.

[Non-patent Document 14] Oji, Y., Miyoshi, Y., Kiyotoh, E., Koga, S., Nakano, Y., Ando, A., Hosen, N., Tsuboi, A., Kawakami, M., Ikegame, K., Oka, Y., Ogawa, H., Noguchi, S., and Sugiyama, H. Absence of mutations in the Wilms' tumor gene WT1 in primary breast cancer. Jpn J Clin Oncol, 34:74-7, 2004.

[Non-patent Document 15] Oji Y, Suzuki T, Nakano Y, Maruno M, Nakatsuka S, Jomgeow T, Abeno S, Tatsumi N, Yokota A, Aoyagi S, Nakazawa T, Ito K, Kanato K, Shirakata T, Nishida S, Hosen N, Kawakami M, Tsuboi A, Oka Y, Aozasa K, Yoshimine T, Sugiyama H, Overexpression of the Wilms' tumor gene WT1 in primary astrocytic tumors. Cancer Sci. 95:822-7, 2004.

[Non-patent Document 16] Oji Y, Yano M, Nakano Y, Abeno S, Nakatsuka S, Ikeba A, Yasuda T, Fujiwara Y, Takiguchi S, Yamamoto H, Fujita S, Kanato K, Ito K, Jomgeow T, Kawakami M, Tsuboi A, Shirakata T, Nishida S, Hosen N, Oka Y, Aozasa K, Monden M, Sugiyama H., Overexpression of the Wilms' tumor gene WT1 in esophageal cancer. Anticancer Res. 24:3103-8, 2004.

[Non-patent Document 17] Oji Y, Nakamori S, Fujikawa M, Nakatsuka S, Yokota A, Tatsumi N, Abeno S, Ikeba A, Takashima S, Tsujie M, Yamamoto H, Sakon M, Nezu R, Kawano K, Nishida S, Ikegame K, Kawakami M, Tsuboi A, Oka Y, Yoshikawa K, Aozasa K, Monden M, Sugiyama H. Overexpression of the Wilms' tumor gene WT1 in pancreatic ductal adenocarcinoma. Cancer Sci. 95:583-7, 2004.

Disclosure of the Invention

An objective of the present invention is to provide molecules that can efficiently suppress WT1 gene expression, and also to provide cell growth-suppressing agents and cell death-inducing agents comprising such a molecule as an active ingredient. In particular, the present invention provides siRNAs, DNAs encoding such siRNAs, and vectors comprising such DNAs, as WT1 gene expression-suppressing molecules.

To accomplish the above-mentioned objective, the present inventors considered suppressing WT1 expression using a vector that allows siRNA, which has attracted attention in recent years as a means for suppressing gene expression, to be expressed in cancer cells. As a result of trial and error, the present inventors discovered that siRNAs, which comprise an RNA

complementary to the WT1 gene transcript and a complementary strand of the RNA, not only suppress WT1 gene expression but also demonstrate a remarkable cell growth-suppressing effect on cancer cell lines. In addition, the present inventors discovered that these siRNAs have effects of inducing mitochondria-mediated cell death and enhancing sensitivity of cancer cells to anticancer agents or cell death-inducing agents.

That is, the present inventors succeeded in developing cell growth-suppressing agents and cell death-inducing agents that utilize WT1-targeting RNAi effects, and therefore completed the present invention.

More specifically, the present invention provides:

[1] a cell growth-suppressing agent comprising any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted;

[2] the cell growth-suppressing agent of [1], wherein the double-stranded RNA comprises an RNA complementary to a 17AA site of a WT1 gene transcript, and an RNA complementary to said RNA;

[3] the cell growth-suppressing agent of [1], wherein the double-stranded RNA comprises an RNA complementary to the nucleotide sequence of SEQ ID NO: 1 present in a 17AA site of a WT1 gene transcript, and an RNA complementary to said RNA;

[4] the cell growth-suppressing agent of [1], wherein the double-stranded RNA comprises the pair of the nucleotide sequence of SEQ ID NO: 1 and the nucleotide sequence of SEQ ID NO: 2;

[5] the cell growth-suppressing agent of [1], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17.

[6] the cell growth-suppressing agent of any one of [1] to [5], wherein the agent targets a cancer cell;

[7] the cell growth suppressing agent of any one of [1] to [5], wherein the agent targets any one of a fibrosarcoma cell, colon cancer cell, leukemia cell, and gastric cancer cell;

[8] a cell death-inducing agent comprising any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene

transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted;

[9] the cell death-inducing agent of [8], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17;

[10] the cell death-inducing agent of [8] or [9], wherein the agent induces cell death through mitochondria;

[11] the cell death-inducing agent of any one of [8] to [10], wherein the agent targets a cancer cell;

[12] the cell death-inducing agent of any one of [8] to [10], wherein the agent targets any one of a fibrosarcoma cell, colon cancer cell, leukemia cell, and gastric cancer cell;

[13] an agent that enhances cancer cell sensitivity to an anticancer agent, wherein the agent comprises any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted;

[14] the agent of [13], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17;

[15] an agent that enhances cancer cell sensitivity to a cell death-inducing agent, wherein the agent comprises any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted;

[16] the agent of [15], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17;

[17] an agent that eliminates mitochondrial membrane potential in a cancer cell, wherein the agent comprises any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted;

[18] the agent of [17], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17;

[19] an agent that enhances cytochrome c release into cytoplasm, wherein the agent comprises any one of (a) to (c) as an active ingredient:

(a) a double-stranded RNA comprising an RNA complementary to a WT1 gene transcript, and an RNA complementary to said RNA;

(b) a DNA encoding the double-stranded RNA of (a); and

(c) a vector into which the DNA of (b) has been inserted; and

[20] the agent of [19], wherein the double-stranded RNA comprises an RNA encoded by the DNA of any one of (a) to (c), and an RNA complementary to said RNA:

(a) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16;

(b) a DNA that hybridizes under stringent conditions with a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 9, 12, 14, and 16; and

(c) a DNA comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15,

and 17.

Brief Description of the Drawings

Fig. 1 shows suppression of HT-1080 cell growth by a vector-based WT1 siRNA.

Fig. 2 is a photograph that shows suppression of 17AA(+) WT1 mRNA expression by a vector-based WT1 siRNA.

Fig. 3 shows the target sites of vector-based WT1 siRNAs.

Fig. 4 shows the structure of vector-based WT1 siRNAs.

Fig. 5 shows photographs that indicate the suppression of WT1 protein expression by vector-based WT1 siRNAs.

Fig. 6 shows suppression of cancer cell growth by vector-based WT1 siRNAs.

Fig. 7 shows suppression of cancer cell growth by vector-based WT1 siRNAs.

Fig. 8 shows the induction of apoptosis in cancer cells by a vector-based WT1 siRNA.

Fig. 9 shows the induction of apoptosis in cancer cells by a vector-based WT1 siRNA.

Fig. 10 shows the loss of mitochondrial membrane potential by a vector-based WT1 siRNA.

Fig. 11 shows the loss of mitochondrial membrane potential by a vector-based WT1 siRNA.

Fig. 12 shows the suppression of cancer cell growth by the combined use of a vector-based WT1 siRNA with anticancer agent doxorubicin.

Fig. 13 shows the suppression of cancer cell growth by the combined use of a vector-based WT1 siRNA with anticancer agent etoposide.

Fig. 14 shows enhancement of the doxorubicin sensitivity of cancer cells by vector-based WT1 siRNAs.

Fig. 15 shows enhancement of the etoposide sensitivity of cancer cells by vector-based WT1 siRNAs.

Fig. 16 is a photograph showing enhancement of the cytochrome c release in cancer cells by the combined use of a vector-based WT1 siRNA with anticancer agents.

Fig. 17 shows enhancement of the loss of the electrons in mitochondrial membrane in cancer cells by the combined use of a vector-based WT1 siRNA with anticancer agents.

Fig. 18 shows enhancement of the loss of the electrons in mitochondrial membrane in cancer cells by the combined use of a vector-based WT1 siRNA with anticancer agents.

Best Mode for Carrying Out the Invention

siRNAs of the present invention are double-stranded RNAs in which an RNA complementary to a transcript of the target WT1 gene (antisense RNA strand) is paired with an

RNA complementary to this RNA (sense RNA strand). The sequence of the WT1 gene transcript that becomes the target of siRNAs of the present invention is not particularly limited so long as the siRNAs can show RNAi effects. Preferably, the sequence exists in the 17AA site of the WT1 gene transcript. As used herein, "17AA site" refers to a site corresponding to 17 amino acids of the WT1 gene transcript sequence in the 5' side site of the two alternative splicing sites present in the WT1 gene. A specific example of such a target sequence includes the sequence of SEQ ID NO: 1. The nucleotide sequences of the sense strand and antisense strand of an siRNA directed against the 17AA site of the WT1 gene transcript used in the Examples are shown in SEQ ID NOs: 1 and 2, respectively. siRNAs of the present invention comprising the nucleotide sequence of SEQ ID NO: 1 paired with the nucleotide sequence of SEQ ID NO: 2 are particularly preferred.

siRNA refers to a short double-stranded RNA chain whose length is in a range that does not show toxicity in cells. Its length is not particularly limited, so long as the length is within a range that does not show toxicity. For example, the length may be 15 to 49 base pairs, and preferably 15 to 30 base pairs.

The portion of the double-stranded RNA where RNAs are paired is not limited to the part that is completely paired, and it may include unpaired portions caused by mismatches (wherein the corresponding nucleotides are not complementary), bulges (wherein one of the strands lacks corresponding nucleotides), and such.

The terminal structure of an siRNA of the present invention may be a blunt end or a sticky (overhanging) end, so long as the structure can suppress WT1 gene expression by RNAi effects. The sticky (overhanging) end structure is not limited to only a structure protruding from the 3' terminal side, and also includes a structure protruding from the 5' terminal side, so long as it is capable of inducing RNAi effects. The number of overhanging nucleotides is not limited to 2 or 3 nucleotides as reported, and can be any number of nucleotides that can induce RNAi effects. For example, the number of nucleotides may be 1 to 8 nucleotides, and preferably 2 to 4 nucleotides. Since this overhanging sequence has low specificity to the WT1 gene transcript, it is not necessary for the sequence to be complementary (antisense) or identical (sense) to the target WT1 gene transcript sequence.

siRNAs of the present invention can be prepared by selecting a target sequence based on the WT1 gene, or preferably a nucleotide sequence of the 17AA(+) isoform. The 17AA(+) isoform refers to an isoform comprising the above-described 17AA. The present inventors have shown that among the four isoforms of WT1, 17AA(+) plays an oncogene-like function (Non-patent Documents 6 and 7). For example, siRNA preparation is carried out by selecting as a target sequence, a continuous region of a transcript mRNA based on the WT1 gene nucleotide sequence, or preferably by selecting the 17AA site region. Double-stranded RNA

corresponding to the selected region can be suitably prepared by methods such as *in vitro* chemical synthesis, *in vitro* transcription using phage RNA polymerase, and performing RNaseIII or Dicer digestion on a long dsRNA transcribed and assembled based on a cloned cDNA. The cDNA sequence of the human WT1 gene used in the Examples is shown in SEQ ID NO: 6. The 17AA site of the WT1 gene corresponds to positions 1137 to 1187 in the sequence of SEQ ID NO: 6. The WT1 gene is registered in NCBI GENBANK as NM_024426.

The siRNAs of the present invention can be prepared by selecting a target sequence based on the nucleotide sequence of an arbitrary site in the WT1 gene.

Examples of a preferred nucleotide sequence in the WT1 gene include positions 1500 to 1529 (SEQ ID NO: 9), positions 2059 to 2088 (SEQ ID NO: 12), positions 2928 to 2957 (SEQ ID NO: 14), and positions 3256 to 3285 (SEQ ID NO: 16) in the WT1 genomic DNA, and nucleotide sequences of DNAs that hybridize under stringent conditions to these sequences. As used herein, the phrase "hybridize under stringent conditions" refers to a situation, where under appropriate stringency hybridization conditions, a nucleic acid molecule with a predetermined sequence (that is, a second polypeptide), when present in a DNA or RNA sample, hybridizes to form a double strand, or inherently binds only to each other. For example, stringent conditions are ordinarily 42°C, 2x SSC, and 0.1% SDS, preferably 50°C, 2x SSC, and 0.1% SDS, and more preferably 65°C, 0.1x SSC, and 0.1% SDS, but are not particularly limited to these conditions. Factors that affect hybridization stringency are considered to be temperature, salt concentration, and a number of other factors, and those skilled in the art can appropriately select these factors to achieve the optimal stringency.

Examples of a DNA that hybridizes under stringent conditions include more preferably DNAs comprising the nucleotide sequence of any one of SEQ ID NOs: 11, 13, 15, and 17.

siRNAs of the present invention can be expressed in cells using a DNA encoding an above-mentioned antisense RNA strand (hereinafter referred to as antisense coding DNA), and a DNA encoding an above-mentioned sense RNA strand (hereinafter referred to as sense coding DNA) (hereinafter, antisense coding DNA and sense coding DNA will be collectively referred to as DNAs of the present invention). The "antisense coding DNA" and "sense coding DNA" can be introduced into the chromosome of a cell with a promoter as they are to intracellularly express antisense RNA and sense RNA, and thereby form siRNA; however, preferably, a vector is made to carry the siRNA expression system so that cells can be transfected efficiently. The "vector" that can be used herein can be selected according to the cell to be transfected and such. For mammalian cells, examples include viral vectors such as retrovirus vector, adenovirus vector, adeno-associated virus vector, vaccinia virus vector, lentivirus vector, herpesvirus vector, alphavirus vector, EB virus vector, papilloma virus vector, and foamyvirus vector, and non-viral vectors including cationic liposome, ligand DNA complex, and gene gun (Y. Niitsu, *et al.*,

Molecular Medicine 35: 1385-1395 (1998)), but are not limited thereto. It is also preferable to use, instead of virus vectors, dumbbell-shaped DNA (Zanta M.A. *et al.*, Gene delivery: a single nuclear localization signal peptide is sufficient to carry DNA to the cell nucleus. Proc Natl Acad Sci U S A. 1999 Jan 5; 96 (1): 91-6), DNA modified to have nuclease resistance, or naked plasmids (Liu F, Huang L. Improving plasmid DNA-mediated liver gene transfer by prolonging its retention in the hepatic vasculature. J. Gene Med. 2001 Nov-Dec; 3(6): 569-76).

The construct for maintaining a DNA encoding an siRNA of the present invention in a vector, may express the antisense RNA strand and sense RNA strand from a same vector or express the respective antisense RNA strand and sense RNA from different vectors. For example, the construct for expressing both antisense RNA and sense RNA from a same vector can be prepared by linking a promoter, such as the pol III system, which is capable of expressing short RNA, to the upstream of an antisense coding DNA and a sense coding DNA, respectively, to form an antisense RNA expression cassette and a sense RNA expression cassette, and inserting these cassettes into a vector either in the same direction or in opposite directions. It is also possible to construct an expression system in which antisense coding DNA and sense coding DNA are placed on different strands in opposite orientations so as to form a pair. This construct is equipped with one double-stranded DNA (siRNA coding DNA) comprising paired antisense RNA coding strand and sense RNA coding strand, and this double-stranded DNA is equipped on both sides with a promoter opposite to each other so as to express antisense RNA and sense RNA from the respective DNA strands. In this case, to avoid addition of excess sequences downstream of the sense RNA and antisense RNA, it is preferable to place a terminator at the 3' end of the respective strands (antisense RNA coding strand and sense RNA coding strand). A continuous sequence of four or more adenine (A) nucleotides may be used as the terminator. In this palindrome expression system, it is preferable to use two different promoters.

A construct that forms a double-stranded RNA comprising a hairpin structure (self-complementary 'hairpin' RNA (hpRNA)) (Smith, N.A. *et al.* Nature, 407:319, 2000; Wesley, S.V. *et al.* Plant J. 27:581, 2001; Piccin, A. *et al.* Nucleic Acids Res. 29:E55, 2001), in which an appropriate sequence (preferably an intron sequence) is inserted between inverted repeats of a target sequence, can be used as a DNA to be inserted into a vector encodes the siRNA of the present invention.

In the present invention, the nucleotide sequence inserted between inverted repeats of a target sequence is not particularly limited, but is preferably, for example, the nucleotide sequence (loop 1) of SEQ ID NO: 18 or the loop sequence AAAACTCGAGAAAA of SEQ ID NO: 3, and more preferably the nucleotide sequence (loop 2) of SEQ ID NO: 19.

A construction for expressing antisense RNA and sense RNA from different vectors may be achieved, for example, by linking a pol III promoter capable of expressing short RNAs to the

upstream of antisense coding DNA and the upstream of sense coding DNA, respectively, to construct an antisense RNA expression cassette and a sense RNA expression cassette, and introducing these cassettes into different vectors.

The "siRNA (double-stranded RNA)-encoding DNA" of the present invention may be a single DNA encoding both strands of an siRNA, or a pair of DNAs encoding each of the strands. The "vector into which the siRNA (double-stranded RNA)-encoding DNA has been inserted" may be a single vector expressing the respective strands of siRNA as two transcripts, a single vector expressing both of the siRNA strands as a single transcript, or two vectors expressing the respective siRNA strands.

It is not necessary for the DNA used in RNAi to be completely identical to the target gene, and it has a sequence identity of at least 70% or more, preferably 80% or more, more preferably 90% or more, and most preferably 95% or more (for example, 96%, 97%, 98%, 99% or more) with the target gene. The sequence identity of nucleotide sequences can be determined using Karlin and Altschul's BLAST algorithm (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). A program called BLASTN has been developed based on this algorithm (Altschul *et al.* J. Mol. Biol. 215: 403-410 (1990)). When nucleotide sequences are analyzed using BLASTN based on BLAST, parameters are set, for example, at score = 100 and wordlength = 12. When using the BLAST and Gapped BLAST programs, the default parameters for the respective programs are used. Specific techniques for these analytical methods are well known.

siRNAs of the present invention, DNAs encoding these siRNAs, and vectors inserted with such DNAs can be individually used as an agent of the present invention as they are, or by mixing with an appropriate compounding agent. By introducing an agent of the present invention into cells using known transfection agents and such, RNAi effects will be exerted in the cells, and effects of the agent of the present invention will be realized.

Examples of the "effects of the agent" of the present invention include cell growth-suppressing effects, cell death-inducing effects, and effects of enhancing the sensitivity of cancer cells to anticancer agents or cell death-inducing agents. Further examples of the effects of the present invention include effects of eliminating mitochondrial membrane potential, and effects of enhancing the cytochrome c release from mitochondria to cytoplasm in cancer cells.

The effects may be temporary effects, or effects that are eventually expressed after a certain amount of time has passed.

Examples of the effects of inducing cell death (apoptosis) in the present invention preferably include effects of inducing the mitochondria-mediated cell death, but are not limited thereto.

When addition of an agent of the present invention to cancer cells is confirmed to eliminate mitochondrial membrane potential and enhance cytochrome c release into the cytoplasm in cancer cells, cell death is considered to be induced.

In the present invention, the anticancer agents which cancer cells have enhanced sensitivity for are not particularly limited, but preferred examples include doxorubicin and etoposide. The cell death-inducing agents of the present invention which cancer cells have enhanced sensitivity for are not particularly limited, but a preferred example is a cancer cell-specific cell death-inducing agent, TRAIL.

Cells in which effects of the agents of the present invention are expected are cells that express the WT1 gene. An example of such cells is cancer cells. More specifically, examples of such cells include cancer cells of leukemia, colon cancer, lung cancer, breast cancer, head and neck squamous cell carcinoma, esophageal cancer, gastric cancer, thyroid cancer, bone and soft tissue sarcoma, ovarian cancer, uterine cancer, kidney cancer, pancreatic cancer, and glioblastoma. Cancer cells of the present invention are not particularly limited in the present invention, but examples preferably include fibrosarcoma cells, colon cancer cells, leukemia cells, and gastric cancer cells, and more preferably include HT-1080, HL-60, SW620, and AZ-521. Therefore, agents of the present invention may be effective not only for academic research, but also as pharmaceuticals for cancer treatment, and especially as pharmaceuticals for cancer treatment targeting the cancers listed above.

When using an agent of the present invention as a pharmaceutical for treating cancer, such an agent can be formulated appropriately. In such formulation, pharmaceutically acceptable compounding ingredients may be mixed. Examples of pharmaceutically acceptable compounding agents include surfactants, excipients, colors, flavors, preservatives, stabilizers, buffers, suspending agents, tonicity adjusting agents, binding agents, disintegrators, lubricants, fluidity enhancers, and corrigents, but are not limited thereto and other conventional carriers may be used appropriately. The types of dosage forms of the above-mentioned formulation include tablets, epipastics, pills, powders, granules, fine granules, soft/hard capsules, film-coated preparations, pellets, sublingual preparations, and paste as oral preparations, and include injections, suppositories, transdermal preparations, ointments, plasters, and liquids for external use as parenteral preparations, and those skilled in the art can select the most appropriate dosage form depending on the administration route, administration target, and such. For *in vivo* administration of a DNA of the present invention, virus vectors such as retroviruses, adenoviruses, or Sendai viruses, or non-viral vectors such as liposomes may be used. Examples of the method of administration include *in vivo* and *ex vivo* methods.

All prior art references cited herein are incorporated by reference into this description.

Examples

The present invention is described in detail below with reference to Examples, but it is not to be construed as being limited thereto.

<Cells used in the Examples>

In the following Examples, four WT1-expressing cell lines: HT-1080 fibrosarcoma cells, AZ-521 gastric cancer cells, SW620 colon cancer cells, and HL-60 promyelocytic leukemia cells; and one non-WT1-expressing cell line: PC-14 lung cancer cells were used. HT-1080, AZ-521, and PC-14 were cultured at 37°C under 5% CO_2in 10% FBS-containing DMEM, and SW620 and HL-60 were cultured in 10% FBS-containing RPMI.

[Example 1] Production of siRNA expression vector that targets the WT1 gene mRNA 17AA site

The DNA to be inserted for generating an siRNA expression vector that targets the WT1 gene mRNA 17 AA site was produced. The specific location of the targeted site was positions 150 to 179 of the WT1 gene sequence shown in SEQ ID NO: 6. The sequence that was produced is shown below (SEQ ID NO: 3):

5'- C CCT TCT GTC CAT TTC ACT GAG CTG GAG CT
(DNA encoding a 30-mer antisense strand of the target RNA)-
-AAAACTCGAGAAAA (loop sequence containing an XhoI site)-
-AG CTC CAG CTC AGT GAA ATG GAC AGA AGG G
(DNA encoding a 30-mer sense strand of the target RNA)-
-GGTACCCCGGATATCTTTTTTT-3'

The DNA was inserted into the cloning site of an siRNA expression vector to produce WRI-4 vector. An siRNA expression vector (pPuro-tRNA-SKE vector), gift from Dr. H. Kawasaki at the Graduate School of Engineering at the University of Tokyo, was used as the siRNA expression vector. The piGENEtRNA Pur Vector (Clontech) may also be used instead of the pPuro-tRNA-SKE vector.

WRI-3 vector was produced as an siRNA expression vector targeting a sequence common to the four isoforms of WT1 gene mRNA. The WRI-3 vector comprises aag gtg gct cct aag ttc atc tga ttc cag (an antisense RNA strand-encoding DNA; SEQ ID NO: 4), and

ctg gaa tca gat gaa ctt agg agc cac ctt (a sense RNA strand-encoding DNA; SEQ ID NO: 5). The site targeted by WRI-3 is positions 1101 to 1130 of the WT1 gene sequence shown in SEQ ID NO: 6.

[Example 2] Cell culturing and introduction of siRNA expression vector

Fibrosarcoma cell line HT-1080 cells that express high levels of the WT1 gene were

cultured in Dulbecco's Modified Medium (DMEM) containing 10%. Trypsinized HT-1080 cells were plated onto a 6-well plate at 2x 10^4 cells/2 ml, and 24 hours later, 2 μg of the WRI-4 vector or an empty vector was introduced into HT-1080 cells using Fugene 6 (ROCHE).

[Example 3] Growth suppression of HT-1080 cells by siRNA expression vector

Cell growth-suppressing effect of the WRI-4 vector was examined. HT-1080 cells transfected with the vector were cultured for 24, 48, or 72 hours, and the number of cells was counted. After trypsinization, the number of cells was calculated using a cytometer.

When an siRNA expression vector directed against WT1 was introduced into HT-1080 cells, growth of the HT-1080 cells was significantly suppressed compared to when an empty control vector was introduced. The results are shown in Fig. 1.

When the WRI-3 expression vector was introduced into HT-1080 cells, and cell growth-suppressing effects were examined, a certain level of cell growth-suppressing effect could be confirmed; however, the effect was weaker than that of the WRI-4 expression vector.

[Example 4] Suppression of WT117AA mRNA expression by siRNA expression vector

Effects of the WRI-4 vector in suppressing WT117AA mRNA expression were examined by RT-PCR.

2 μg of the WRI-4 RNAi expression vector directed against the 17AA site of WT1, or an empty vector, was introduced into HT-1080 cells (2x 10^4 cells) by Lipofection using Fugene 6 (Roche). Cells were collected 96 hours after the introduction. The cells were then trypsinized and washed twice with PBS. Then, total RNA was extracted using Trizol, and cDNA was synthesized in the presence of MMLV reverse transcriptase using 2 μg of the total RNA as template and dT primer. Next, PCR was performed using forward primer 5'- gac ctg gaa tca gat gaa ctt ag -3' (SEQ ID NO: 7) and reverse primer 5'- gag aac ttt cgc tga caa gtt -3' (SEQ ID NO: 8), which are designed to sandwich the 17AA site of WT1, the PCR products were subjected to electrophoresis on an agarose gel, and expression of the WT1 17AA(+) and 17AA(-) mRNA was examined.

The results are shown in Fig. 2. Decrease of the 17AA(+)WT1 mRNA expression was observed in cells transfected with the WRI-4 expression vector.

[Example 5] Construction of siRNA vectors

One type of an oligonucleotide whose sequence is specific to WT1 mRNA and comprises a loop 1 sequence (40 nt, SEQ ID NO: 18) (sense strand (30 nt) - loop 1 (40 nt, SEQ ID NO: 18) - antisense strand (30 nt)), and five types of an oligonucleotide whose sequence is specific to WT1 mRNA and comprises a loop 2 sequence (10 nt: the loop sequence of human

pre-miR-23, SEQ ID NO: 19) (sense strand (30 nt) - loop 2 (10 nt, SEQ ID NO: 19) - antisense strand (30 nt)) were synthesized (Japan Bio Service). After annealing these oligonucleotides, they were inserted downstream of the $tRNA^{Val}$ promoter of the piGENEtRNA Pur Vector (Clonetech) to produce a total of six types of siRNA vectors, loop1-WRI-4 that transcribes dsRNA comprising loop1 (40 nt, SEQ ID NO: 18), and WRI-4, WRI-4m, WRI-16m, WRI-17m, and WRI-18m, which transcribe dsRNA comprising loop 2 (10 nt). Among them, those indicated with m are vectors carrying a sequence, into which mutations were inserted to the sense strand to increase the effect of vector-based WT1 siRNAs. The target site and sequence of each of the siRNA vectors are shown in Fig. 3, Fig. 4, and Table 1.

Table 1

siRNA Vector		Sequence[a]	SEQ ID NO	Loop[b]	Position in WT1
loop1- WRI-4	Target Sequence	AGCTCCAGCTCAGTGAAATGGACAGAAGGG	9	loop 1	1500-1529
	Sense sequence	AGCTCCAGCTCAGTGAAATGGACAGAAGGG	10		
WRI-4	Target Sequence	AGCTCCAGCTCAGTGAAATGGACAGAAGGG	9	loop 2	1500-1529
	Sense sequence	AGCTCCAGCTCAGTGAAATGGACAGAAGGG	10		
WRI-4m	Target Sequence	AGCTCCAGCTCAGTGAAATGGACAGAAGGG	9	loop 2	1500-1529
	Sense sequence	AGCTCCAGCTTAGTGAAGTGGGTAGGAGGG	11		
WRI-16m	Target Sequence	AAACATGACCAAACTCCAGCTGGCGCTTTG	12	loop 2	2059-2088
	Sense sequence	AAACATGACCAAACTCTAGTTGGTGCTTTG	13		
WRI-17m	Target Sequence	AACCATGCTGGTATATGGCTTCAAGTTGTA	14	loop 2	2928-2957
	Sense sequence	AACCATGCTGGTATATGGCTTTAGGTTGTG	15		
WRI-18m	Target Sequence	AAGTACTAGATGCATCACTGGGTGTTGATC	16	loop 2	3256-3285
	Sense sequence	AAGTACTAGATGCATCATTGGGTGTTGGTT	17		

a: Underlines in the sense sequences indicate insertion of mutations.
b: The sequence of loop 1 is AAAACTCGAGAAAAAAGGGAGCACAACCATCTGCATTTGAGAGG (SEQ ID NO: 18), and the sequence of loop 2 is CTTCCTGTCA (SEQ ID NO: 19).

[Example 6] Suppression of WT1 gene expression by vector-based WT1 siRNA

Efficiency of suppression of WT1 gene expression in HT-1080 fibrosarcoma cells was examined for the six types of vector-based WT1 siRNAs targeting various sites in WT1 mRNA: loop 1-WRI-4, WRI-4, WRI-4m, WRI-16m, WRI-17m, and WRI-18m, and a mixture of WRI-4m, WRI-16m, WRI-17m, and WRI-18m (Fig. 3, Fig. 4, and Table 1).

HT-1080 cells were treated with the six vector-based WT1 siRNAs and a mock vector, respectively, and 72 hours later, the WT1 protein expression levels were analyzed by Western blotting.

Treatments with the siRNA vectors and mock vector were carried out in the following steps. Cells were plated onto a 6-well plate, and on the next day, the WT1-siRNA expression vectors and mock vector were transiently expressed by lipofection using FuGENE 6 (Roche). Three days later, the cells were trypsinized and the number of cells was counted. The WT1 protein expression level in these cells was analyzed by Western blotting.

Western blot analysis was carried out by the following steps. Cells transiently expressing the siRNA expression vectors and mock vector were dissolved in an SDS sample buffer, and proteins were separated by SDS-PAGE and then blotted onto a PVDF membrane. Color was developed using a BCIP-NBT kit with the anti-WT1 antibody C-19 (Santa Cruz Biotechnology), an anti-cytochrome C antibody (Pharmingen), or an anti-GAPDH antibody (Chemicon) as a primary antibody, and an ALP-conjugated anti-rabbit or anti-mouse antibody (Santa Cruz Biotechnology) as a second antibody.

Results of the Western blot analysis showed that expression of the WT1 protein is decreased by all of the WT1-targeting vector-based WT1 siRNAs. Herein, when treated with WRI-4, WRI-4m, WRI-16m, WRI-18m, and WRI-4m + 16m + 17m + 1m8, the protein expression level decreased to 10 to 20% in comparison with cells transfected with a mock vector; however, when treated with loop1-WRI-4 and WRI-17, the extent of decrease in WT1 protein expression was small (Fig. 5).

[Example 7] WT1-specific growth suppression of tumor cells by vector-based WT1 siRNA

To analyze the effect of vector-based WT1 siRNAs on cell growth, the number of cells was counted 72 hours after introducing the six types of vector-based WT1 siRNAs, loop1-WRI-4,

WRI-4, WRI-4m, WRI-16m, WRI-17m, and WRI-18m, and a mixture of WRI-4m, WRI-16m, WRI-17m, and WRI-18m, respectively. In HT-1080 fibrosarcoma cells (an WT1-expressing cell line), all of the WT1 siRNA treatments significantly suppressed cell growth compared to mock vector treatment. Among the WT1 siRNAs, WRI-4m suppressed growth by 90% or more. In contrast, in PC-14 lung cancer cells (a non-WT1-expressing cell line), cell growth was not suppressed by any of the six vector-based WT1 siRNA treatments (Fig. 6).

Furthermore, to investigate whether two types of vector-based WT1 siRNAs (WRI-4m and WRI-16m) can suppress the growth of various WT1-expressing cancer cells, these vectors were introduced into three WT1-expressing cell lines: AZ-521 gastric cancer cells, SW620 colon cancer cells, and HL-60 leukemia cells, and the number of cells were counted 72 hours later.

The results showed that in all three types of the WT1-expressing cancer cells, WRI-4m and WRI-16m treatments significantly suppressed growth compared to mock vector treatment (Fig. 7).

[Example 8] Induction of apoptosis by vector-based WT1 siRNA

To elucidate the mechanism of cancer cell growth suppression by vector-based WT1 siRNAs, induction of apoptosis in cells subjected to a vector-based WT1 siRNA treatment was analyzed. Two WT1-expressing cell lines HT-1080 and AZ-521, and a non-WT1-expressing cell line PC-14 were subjected to the WRI-4m treatment, double-stained with AnnexinV-FITC and PI, and then analyzed by flow cytometry.

Apoptosis analysis by flow cytometry was carried out by the following steps. First, to detect apoptosed cells, 1.0x 10^5 cells were washed with PBS, and then the cells were stained by reaction with Annexin V-FITC and PI at room temperature for 15 minutes, using the MEBCYTO Apoptosis kit (Medical and Biological Laboratories Co., Ltd, Nagoya, Japan). Upon analysis of these cells using a FACScan flowcytometer (Becton Dickinson, San Jose, CA), Annexin V-FITC-positive cells were defined as apoptosed cells.

As a result, the WRI-4m treatment induced apoptosis in 71.1% and 40.6% of the WT1-expressing cell lines HT-1080 cells and AZ-521 cells, respectively. In contrast, in the non-WT1-expressing cell line PC-14, WRI-4m treatment did not induce apoptosis (Figs. 8 and 9).

[Example 9] Loss of mitochondrial membrane potential by vector-based WT1 siRNA

To elucidate whether the vector-based WT1 siRNA-induced apoptosis takes place through a mitochondria-mediated pathway, the WT1-expressing cell line HT-1080 cells and the non-WT1-expressing cell line PC14 cells were both treated with WRI-4m and a mock vector respectively. 72 hours later, the state of mitochondrial membrane potential was analyzed by

MitoLight staining followed by flow cytometry.

The change in mitochondrial membrane potential ($\Delta\Psi m$) due to apoptosis induction was analyzed using the MitoLight apoptosis detection kit (Chemicon). Cells after apoptosis induction were incubated at 37°C in a buffer containing MitoLight (a mitochondria staining dye) for 15 minutes, and then analyzed on a FACScan FL2 channel.

As a result, compared to the mock vector treatment, the WRI-4m treatment significantly induced loss of the mitochondrial membrane potential in HT-1080 (a WT1-expressing cell line). However, the WRI-4m treatment did not induce loss of the mitochondrial membrane potential in the non-WT1-expressing cell line PC-14 (Figs. 10 and 11). These results indicated that apoptosis induction by vector-based WT1 siRNA takes place through a mitochondria-mediated pathway.

[Example 10] Enhancement of cell growth suppression through combined use of vector-based WT1 siRNA with anti-cancer agents

Most anticancer agents induce apoptosis in cancer cells through a mitochondria-mediated pathway. Therefore, the present inventors thought that the sensitivity of cancer cells to anticancer agents may be enhanced by using chemotherapeutic agents in combination with a vector-based WT1 siRNA that eliminates the mitochondrial membrane potential. Accordingly, cell growth suppression by anticancer agents doxorubicin and etoposide in cells treated with a vector-based WT1 siRNA (WRI-4m or WRI-16m) and untreated cells was analyzed.

Combined use of an siRNA vector with a chemotherapeutic agent or a death ligand, was carried out by the following steps. Cells were plated onto a 6-well plate, and on the next day, the vector-based WT1 siRNA and mock vector were transiently expressed by lipofection using FuGENE 6 (Roche), and 48 hours later, the cells were treated for another 24 hours with 25 μM etoposide (WAKO), 0.2 μM doxorubicin (Sigma), or 50 mg/mL of TNF-related apoptosis-inducing ligand (TRAIL) (Peprotech).

The results showed that suppression of HT-1080 cell growth is greater when vector-based WT1 siRNA is used in combination with doxorubicin or etoposide than when only doxorubicin or etoposide is used (Figs. 12 and 13).

Furthermore, to analyze the cell sensitivity to anticancer agents after vector-based WT1 siRNA treatment, difference in the number of cells counted after combined treatment and after the vector treatment alone was calculated as a percentage relative to the number of cells counted after the vector treatment alone. The results showed that sensitivity to doxorubicin and etoposide is enhanced by vector-based WT1-siRNA treatment in HT-1080 cells, as indicated in Figs. 14 and 15.

[Example 11] Enhancing the induction of mitochondria-mediated apoptosis by combined use of vector-based WT1 siRNA with an anticancer agent

To reveal that enhancement of cell growth suppression due to combined use of vector-based WT1-siRNA with an anticancer agent is caused by enhancing the induction of mitochondria-mediated apoptosis, the release of cytochrome c from mitochondria into cytoplasm which takes place after combined treatment of vector-based WT1-siRNA with doxorubicin or etoposide was analyzed.

The release of cytochrome c from mitochondria into cytoplasm was analyzed by the following steps. Cells were washed with PBS, dissolved in ice-cooled STE buffer (250 mM sucrose, 25 mM Tris, and 1 mM EDTA, pH6.8), and then centrifuged at 15,000 rpm for 15 minutes. The supernatant was mixed with an equal amount of 2x Laemieli's SDS sample buffer, and then stored at -20°C until it was used in Western blot analysis.

The analysis results showed that the release of cytochrome c into cytoplasm is enhanced by combined treatment of WRI-4m with the respective agents, as shown in Fig. 16.

Mitochondrial membrane potential after combined treatment using vector-based WT1 siRNA with doxorubicin, etoposide, and TRAIL, respectively, was evaluated by flow cytometry. Compared to treatment of an anticancer agent alone, combined treatment of WRI-4m with doxorubicin or etoposide significantly enhanced the loss of mitochondrial membrane potential (Figs. 17 and 18).

When effects of the combined use of TRAIL, an attractive cancer-specific apoptosis-inducing agent, with a vector-based WT1 siRNA were analyzed, release of cytochrome c was enhanced (Fig. 16) and loss of mitochondrial membrane potential was enhanced (Figs. 17 and 18) after the combined treatment, as with the combined use of a vector-based WT1 siRNA with doxorubicin or etoposide.

Industrial Applicability

The present invention provides siRNA that can efficiently suppress WT1 gene expression, and cell growth-suppressing agents comprising such siRNA as an active ingredient. It also provids cell death-inducing agents comprising such siRNA as an active ingredient, and agents that enhance the sensitivity of cancer cells to anticancer agents and cell death-inducing agents.

Since the WT1 gene is known to be highly expressed in cancer cells, the agents of the present invention are particularly useful as novel anticancer agents. Furthermore, since the agents of the present invention comprising siRNA as an active ingredient have functions of enhancing the effects of conventional anticancer agents, they are further expected to improve

conventional anticancer drug therapy.